

SCORE Search Results Details for Application 10573229 and Search Result 20090528_121050_us-10-573-229a-1.rng.

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This page gives you Search Results detail for the Application 10573229 and Search Result 20090528_121050_us-10-573-229a-1.rng.

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GenCore version 6.3
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OM nucleic - nucleic search, using sw model

Run on: May 31, 2009, 21:45:58 ; Search time 320 Seconds
(without alignments)
47647.773 Million cell updates/sec

Title: US-10-573-229A-1
Perfect score: 920
Sequence: 1 tctgtagaggggaatggctg.....acccccaaagaaaccttcta 920

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 14112681 seqs, 8286569208 residues

Total number of hits satisfying chosen parameters: 28225362

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_200812:*
1: geneseqn1:*
2: geneseqn2:*
3: geneseqn3:*
4: geneseqn4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				DB	ID	Description
	No.	Score	Query	Match	Length				

	1	920	100.0		920		2	ADZ14485	Adz14485 DNA encod
	2	920	100.0		920		3	AEL40763	Ael40763 Human tum
c	3	178.2	19.4		390		2	ADZ14751	Adz14751 ORF DNA e
c	4	176.6	19.2		390		3	AEL41029	Ael41029 Human tum
	5	122.6	13.3		561		1	ADY36463	Ady36463 HIRA geno
	6	122.6	13.3		561		1	ADS31075	Ads31075 Human gen
	7	121.2	13.2		541		1	ADY36462	Ady36462 HIRA geno
	8	121.2	13.2		541		1	ADS31074	Ads31074 Human gen
	9	104.8	11.4		737		1	ADC20771	Adc20771 Human sec
	10	104.8	11.4		737		1	ADA44374	Ada44374 Human sec
	11	104.8	11.4		737		1	ADF10918	Adf10918 Human sec
	12	104.8	11.4		737		1	ADA98650	Ada98650 Human sec
	13	104.8	11.4		737		3	AOD72587	Aod72587 Human sec
	14	104.8	11.4		797		1	AAC79717	Aac79717 Human sec
	15	104.8	11.4		797		1	ADC20168	Adc20168 Human sec
	16	104.8	11.4		797		1	ADA43908	Ada43908 Human sec
	17	104.8	11.4		797		1	ADF10604	Adf10604 Human sec
	18	104.8	11.4		797		1	ADA98008	Ada98008 Human sec
	19	104.8	11.4		797		3	AOD66200	Aod66200 Human sec
	20	104.8	11.4		797		4	ATC73738	Atc73738 Human sec
c	21	104.8	11.4	137000			2	ADH77370	Adh77370 Human PTP
c	22	104.8	11.4	137000			3	AEE96219	Aee96219 Human PTP
	23	104.2	11.3		744		2	AGE46923	Age46923 Human sin
c	24	101.8	11.1	138244			2	AEX41464	Aex41464 Human rhe
c	25	101.2	11.0		6000		4	ATN10540	Atn10540 Human tra
c	26	98.4	10.7	84105			2	AFS52981	Afs52981 Human pol
c	27	98	10.7	55927			2	AFI73361	Afi73361 Human gen
c	28	97.8	10.6	9245			2	AFI71693	Afi71693 Human gen
c	29	97.8	10.6	9245			2	AFI71694	Afi71694 Human gen
	30	97.4	10.6	10252			1	AAS31966	Aas31966 Human liv
	31	97.4	10.6	10252			1	AAK90931	Aak90931 Human dig
	32	97.4	10.6	10252			1	ABN90321	Abn90321 Human liv
	33	97.4	10.6	10252			1	ADJ15234	Adj15234 Human liv
c	34	97.4	10.6	142439			4	ATR89011	Atr89011 Human can
	35	95.4	10.4		3361		2	ADQ64498	Adq64498 Novel hum
c	36	93.6	10.2	153170			2	ADQ17382	Adq17382 Human sof
c	37	92.2	10.0	101099			3	AEG93597	Aeg93597 Human tum
c	38	91.8	10.0	143550			2	AFI72487	Afi72487 Human gen
	39	91.4	9.9		1399		4	ARY86811	Ary86811 Psoriasis
	40	91.4	9.9		1410		4	ARY86813	Ary86813 Psoriasis
	41	91.4	9.9		1458		4	ARY86809	Ary86809 Psoriasis
	42	91.4	9.9	173805			1	ADL13775	Adl13775 Osteoarth
	43	91.4	9.9	215308			3	ASQ09904	Asq09904 Human CTD

44	90.8	9.9	76118	2	AFI73937	Afi73937 Human gen
45	90.8	9.9	92117	1	ACN44746	Acn44746 Human gen

ALIGNMENTS

RESULT 1

ADZ14485

ID ADZ14485 standard; DNA; 920 BP.

XX

AC ADZ14485;

XX

DT 11-JUN-2007 (revised)

DT 16-JUN-2005 (first entry)

XX

DE DNA encoding a human tumor associated antigen Seq 1.

XX

KW chromosome 6; tumor-associated antigen; antisense therapy;

KW RNA interference; diagnosis; cytostatic; cancer; metastasis; gene; ds.

XX

OS Homo sapiens.

XX

PN WO2005030250-A2.

XX

PD 07-APR-2005.

XX

PF 23-SEP-2004; 2004WO-EP010697.

XX

PR 26-SEP-2003; 2003DE-01044799.

XX

PA (GANY-) GANYMED PHARM AG.

XX

PI Tuereci O, Sahin U, Helftenbein G, Schlueter V;

XX

DR WPI; 2005-285105/29.

DR P-PSDB; ADZ14486.

DR PC:NCBI; gi22697845.

XX

PT Compositions for treating and diagnosing cancer, contain agents that
 PT inhibit activity or expression of specific tumor-associated antigens, or
 PT bind to these antigens or nucleic acid encoding them.

XX

PS Claim 1; SEQ ID NO 1; 388pp; German.

XX

CC This invention relates to a novel pharmaceutical composition which
 CC comprises an agent that inhibits the activity or expression of a specific
 CC tumor-associated antigen (TAg). Specifically, it relates to tumor-
 CC associated antigens that are encoded by one of the following 75 nucleic

CC acids sequences, fragments or derivatives thereof as given in the
CC specification. The present invention describes antisense nucleic acids
CC that hybridize to these TAg polynucleotides that may be used for
CC antisense therapy and RNA interference, as well as methods for diagnosing
CC a disease associated with (abnormal) expression of TAg. Accordingly, it
CC further relates to methods for determining regression, progression and
CC onset of a disease by administering an antibody, optionally linked to a
CC therapeutic or diagnostic agent, that binds to TAg. As such, cytostatic
CC compositions derived thereof are used for treating a wide range of
CC cancers and their metastases, where the agents that bind specifically to
CC TAg, and the nucleic acids that encode them, are useful for diagnosis and
CC monitoring. This polynucleotide is a human DNA sequence encoding a tumor
CC associated antigenic protein of the invention.

CC Revised record issued on 11-JUN-2007 : Enhanced with precomputed
CC information from BOND.

XX

SQ Sequence 920 BP; 238 A; 255 C; 255 G; 172 T; 0 U; 0 Other;

Query Match 100.0%; Score 920; DB 2; Length 920;
Best Local Similarity 100.0%; Pred. No. 2.3e-273;
Matches 920; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	TCTGTAGAGGGGAATGGCTGCTGTGTCATGGGGGTGCATGAGCAGCCCAGTGGAGAGGTG	60
Db	1	TCTGTAGAGGGGAATGGCTGCTGTGTCATGGGGGTGCATGAGCAGCCCAGTGGAGAGGTG	60
Qy	61	CACTTGGTGAGAAACCGATGCCTCTGCCAACACCTGCACTAACCTGCTGGGTCTGAGAC	120
Db	61	CACTTGGTGAGAAACCGATGCCTCTGCCAACACCTGCACTAACCTGCTGGGTCTGAGAC	120
Qy	121	TGAGCCACTTTGGAAGCTGATCTTGGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCAC	180
Db	121	TGAGCCACTTTGGAAGCTGATCTTGGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCAC	180
Qy	181	AGCCAACAACAAGACTGCAACCTCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATT	240
Db	181	AGCCAACAACAAGACTGCAACCTCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATT	240
Qy	241	GCTCCTTGATTCTTAACCCACAGAAATTGTGTAAGACCTCCATCAGGTGTCGACAAGGAA	300
Db	241	GCTCCTTGATTCTTAACCCACAGAAATTGTGTAAGACCTCCATCAGGTGTCGACAAGGAA	300
Qy	301	GATCCCAGTAGGGCAGGAGACAGGAGCACCTCTGCTGTGGCCAATGCAGGAATGCTGGCC	360
Db	301	GATCCCAGTAGGGCAGGAGACAGGAGCACCTCTGCTGTGGCCAATGCAGGAATGCTGGCC	360
Qy	361	ATCATTGCTTCTGCTGGGCGACTGAGAAGCATCACCCACTTCCCCAGAACCTTTTTTACG	420

Db	361	ATCATTGCTTCTGCTGGGCGACTGAGAAGCATCACCCACTTCCCCAGAACCTTTTTTTACG	420
Qy	421	TGGAGTGAAAACTTTAAGGGGCTGTCCAGCTAAACCTCCAACCTCCAGATCCCATGCCAA	480
Db	421	TGGAGTGAAAACTTTAAGGGGCTGTCCAGCTAAACCTCCAACCTCCAGATCCCATGCCAA	480
Qy	481	TTTCTCTGCTTCTGCAAAAGGACTTCAAGTGAAAGACATCTGCAGCTGTGAACGGGGGTA	540
Db	481	TTTCTCTGCTTCTGCAAAAGGACTTCAAGTGAAAGACATCTGCAGCTGTGAACGGGGGTA	540
Qy	541	AAACCCTCCCTGCCCCAGGCCCAAGCAAGGATTTCCCTAGCGGGGAGGAAGGTAGAATC	600
Db	541	AAACCCTCCCTGCCCCAGGCCCAAGCAAGGATTTCCCTAGCGGGGAGGAAGGTAGAATC	600
Qy	601	GAGAGACCTCTAACCCTGGGAGAGGAGGGAGGGAAATCTCCGAGGACCAGGGTTATGCAA	660
Db	601	GAGAGACCTCTAACCCTGGGAGAGGAGGGAGGGAAATCTCCGAGGACCAGGGTTATGCAA	660
Qy	661	CAACACAAGGGAAGTACCTGCTGGGTCTGGGGGTGGGGAAGGAAAATCCCTACTGCCC	720
Db	661	CAACACAAGGGAAGTACCTGCTGGGTCTGGGGGTGGGGAAGGAAAATCCCTACTGCCC	720
Qy	721	CAAGAGCCAGCCCCGAACCAAGGCACAGCTTATACTGGCCCCGGGGCCTGGGGGGGCAC	780
Db	721	CAAGAGCCAGCCCCGAACCAAGGCACAGCTTATACTGGCCCCGGGGCCTGGGGGGGCAC	780
Qy	781	GAAAACCTTGAAAAAGGGGCGCCTTCCCAGCTTCCCCGGGGGTAAGGGCTTTACCCCCCA	840
Db	781	GAAAACCTTGAAAAAGGGGCGCCTTCCCAGCTTCCCCGGGGGTAAGGGCTTTACCCCCCA	840
Qy	841	GAGGGGGGGGGGAAAAATCCGAGTGGGATCTTTCCCAACCGCCGAAGACTAAAACCTTTAA	900
Db	841	GAGGGGGGGGGGAAAAATCCGAGTGGGATCTTTCCCAACCGCCGAAGACTAAAACCTTTAA	900
Qy	901	ACCCCCAAAGAAACCTTCTA	920
Db	901	ACCCCCAAAGAAACCTTCTA	920

RESULT 2
AEL40763
ID AEL40763 standard; DNA; 920 BP.
XX
AC AEL40763;
XX
DT 11-JUN-2007 (revised)
DT 11-JAN-2007 (first entry)
XX
DE Human tumor-associated DNA SEQ ID NO 1.

antigen; tumor; neoplasm; diagnosis; therapeutic; cytostatic;
tumor-associated antigen; colon tumor; rectal tumor; renal tumor;
adrenal tumor; breast tumor; prostate tumor; uterus tumor; ovary tumor;
endometroid carcinoma; esophagus tumor; liver tumor; pancreas tumor;
skin tumor; brain tumor; lung tumor; lymphoma; nervous system tumor;
carcinoma; chromosome-6; gene; ds.

Homo sapiens.

WO2006100089-A2.

28-SEP-2006.

23-MAR-2006; 2006WO-EP002695.

24-MAR-2005; 2005DE-10013846.

(GANY-) GANYMED PHARM AG.

Sahin U, Tuereci O, Koslowski M, Helftenbein G, Usener D;
Schlueter V;

WPI; 2006-789387/80.
P-PSDB; AEL40764.
PC:NCBI; gi22697845.

Pharmaceutical composition containing inhibitors of specific tumor-
associated antigens, useful for treating cancers, also diagnosis and
monitoring using antigen-specific reagents.

Claim 1; SEQ ID NO 1; 398pp; German.

This invention describes a novel method of identifying surface-associated
antigens for tumor diagnosis and therapy whereby tumor-associated genetic
products are identified and treated. The therapy and diagnosis applies to
diseases in which the tumor-associated products are aberrantly expressed,
i.e. proteins, polypeptides and peptides expressed in association with
the tumor and it encodes nucleic acids for said proteins, polypeptides and
peptides. The novel process has applications in medicine, particularly
oncology and can be used to make pharmaceuticals for the therapy of
colon, rectal, kidney, adrenal glands, breast, prostate, uterus, ovary,
endometrial, esophagus, blood, liver, pancreas, skin, brain, lung
cancers, lymphoma, neuroblastoma or other carcinomas. This sequence
encodes a tumor-associated protein used in the method of the invention
which is localized on chromosome 6 (6q26-27).

Revised record issued on 11-JUN-2007 : Enhanced with precomputed
information from BOND.

XX					
SQ	Sequence 920 BP; 238 A; 255 C; 255 G; 172 T; 0 U; 0 Other;				
	Query Match 100.0%; Score 920; DB 3; Length 920;				
	Best Local Similarity 100.0%; Pred. No. 2.3e-273;				
	Matches 920; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Qy	1	TCTGTAGAGGGGAATGGCTGCTGTGTCATGGGGGTGCATGAGCAGCCCAGTGGAGAGGTG	60		
Db	1	TCTGTAGAGGGGAATGGCTGCTGTGTCATGGGGGTGCATGAGCAGCCCAGTGGAGAGGTG	60		
Qy	61	CACTTGGTGAGAAACCGATGCCTCTGCCAACCACCTGCACTAACCTGCTGGGTCTGAGAC	120		
Db	61	CACTTGGTGAGAAACCGATGCCTCTGCCAACCACCTGCACTAACCTGCTGGGTCTGAGAC	120		
Qy	121	TGAGCCACTTTGGAAGCTGATCTTGGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCAC	180		
Db	121	TGAGCCACTTTGGAAGCTGATCTTGGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCAC	180		
Qy	181	AGCCAACAACAAGACTGCAACCTCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATT	240		
Db	181	AGCCAACAACAAGACTGCAACCTCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATT	240		
Qy	241	GCTCCTTGATTCTTAACCCACAGAAATTGTGTAAGACCTCCATCAGGTGTCGACAAGGAA	300		
Db	241	GCTCCTTGATTCTTAACCCACAGAAATTGTGTAAGACCTCCATCAGGTGTCGACAAGGAA	300		
Qy	301	GATCCCAGTAGGGCAGGAGACAGGAGCACCTCTGCTGTGGCCAATGCAGGAATGCTGGCC	360		
Db	301	GATCCCAGTAGGGCAGGAGACAGGAGCACCTCTGCTGTGGCCAATGCAGGAATGCTGGCC	360		
Qy	361	ATCATTGCTTCTGCTGGGCGACTGAGAAGCATCACCCACTTCCCCAGAACCTTTTTTTACG	420		
Db	361	ATCATTGCTTCTGCTGGGCGACTGAGAAGCATCACCCACTTCCCCAGAACCTTTTTTTACG	420		
Qy	421	TGGAGTGAAAACTTTAAGGGGCTGTCCAGCTAAACCTCCAACCTCCAGATCCCATGCCAA	480		
Db	421	TGGAGTGAAAACTTTAAGGGGCTGTCCAGCTAAACCTCCAACCTCCAGATCCCATGCCAA	480		
Qy	481	TTTCTCTGCTTCTGCAAAAAGGACTTCAAGTGAAAGACATCTGCAGCTGTGAACGGGGGTA	540		
Db	481	TTTCTCTGCTTCTGCAAAAAGGACTTCAAGTGAAAGACATCTGCAGCTGTGAACGGGGGTA	540		
Qy	541	AAACCCTCCCTGCCCCAGGCCCAAGCAAGGATTTCCCTAGCGGGGAGGAAGGTAGAATC	600		
Db	541	AAACCCTCCCTGCCCCAGGCCCAAGCAAGGATTTCCCTAGCGGGGAGGAAGGTAGAATC	600		
Qy	601	GAGAGACCTCTAACCCTGGGAGAGGAGGGAGGGAAATCTCCGAGGACCAGGGTTATGCAA	660		

Db	601	GAGAGACCTCTAACCCCTGGGAGAGGAGGGAGGGGAAATCTCCGAGGACCAGGGTTATGCAA	660
Qy	661	CAACACAAGGGAAGTACCTGCTGGGTCTGGGGGTTGGGGAAGGAAAATCCCTACTGCCC	720
Db	661	CAACACAAGGGAAGTACCTGCTGGGTCTGGGGGTTGGGGAAGGAAAATCCCTACTGCCC	720
Qy	721	CAAGAGCCAGCCCCGAACCCAAGGCACAGCTTATACTGGCCCCGGGGCCTGGGGGGGCAC	780
Db	721	CAAGAGCCAGCCCCGAACCCAAGGCACAGCTTATACTGGCCCCGGGGCCTGGGGGGGCAC	780
Qy	781	GAAAACCTTGAAAAAGGGGCGCCTTCCCAGCTTCCCCGGGGGTAAGGGCTTTACCCCCCA	840
Db	781	GAAAACCTTGAAAAAGGGGCGCCTTCCCAGCTTCCCCGGGGGTAAGGGCTTTACCCCCCA	840
Qy	841	GAGGGGGGGGGGAAAAATCCGAGTGGGATCTTTCCCAACCGCCGAAGACTAAAACCTTTAA	900
Db	841	GAGGGGGGGGGGAAAAATCCGAGTGGGATCTTTCCCAACCGCCGAAGACTAAAACCTTTAA	900
Qy	901	ACCCCCAAAGAAACCTTCTA	920
Db	901	ACCCCCAAAGAAACCTTCTA	920

RESULT 3

ADZ14751/c

ID	ADZ14751 standard; DNA; 390 BP.
XX	
AC	ADZ14751;
XX	
DT	16-JUN-2005 (first entry)
XX	
DE	ORF DNA encoding a human tumor associated antigen Seq 267.
XX	
KW	chromosome 6; tumor-associated antigen; antisense therapy;
KW	RNA interference; diagnosis; cytostatic; cancer; metastasis; gene; ds.
XX	
OS	Homo sapiens.
XX	
PN	WO2005030250-A2.
XX	
PD	07-APR-2005.
XX	
PF	23-SEP-2004; 2004WO-EP010697.
XX	
PR	26-SEP-2003; 2003DE-01044799.
XX	
PA	(GANY-) GANYMED PHARM AG.
XX	
PI	Tuereci O, Sahin U, Helftenbein G, Schlueter V;

XX

XX

XX

XX

Query Match 19.4%; Score 178.2; DB 2; Length 390;
Best Local Similarity 93.5%; Pred. No. 6.7e-44;
Matches 186; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Db 84 GGGCAGCGTTATCCACAGC 66

RESULT 4

AEL41029/c

ID AEL41029 standard; DNA; 390 BP.

XX

AC AEL41029;

XX

DT 11-JAN-2007 (first entry)

XX

DE Human tumor-associated DNA SEQ ID NO 267.

XX

KW antigen; tumor; neoplasm; diagnosis; therapeutic; cytostatic;

KW tumor-associated antigen; colon tumor; rectal tumor; renal tumor;

KW adrenal tumor; breast tumor; prostate tumor; uterus tumor; ovary tumor;

KW endometroid carcinoma; esophagus tumor; liver tumor; pancreas tumor;

KW skin tumor; brain tumor; lung tumor; lymphoma; nervous system tumor;

KW carcinoma; chromosome-6; gene; ds.

XX

OS Homo sapiens.

XX

PN WO2006100089-A2.

XX

PD 28-SEP-2006.

XX

PF 23-MAR-2006; 2006WO-EP002695.

XX

PR 24-MAR-2005; 2005DE-10013846.

XX

PA (GANY-) GANYMED PHARM AG.

XX

PI Sahin U, Tuereci O, Koslowski M, Helftenbein G, Usener D;

PI Schlueter V;

XX

DR WPI; 2006-789387/80.

DR P-PSDB; AEL41030.

XX

PT Pharmaceutical composition containing inhibitors of specific tumor-

PT associated antigens, useful for treating cancers, also diagnosis and

PT monitoring using antigen-specific reagents.

XX

PS Claim 1; SEQ ID NO 267; 398pp; German.

XX

CC This invention describes a novel method of identifying surface-associated

CC antigens for tumor diagnosis and therapy whereby tumor-associated genetic

CC products are identified and treated. The therapy and diagnosis applies to

CC diseases in which the tumor-associated products are aberrantly expressed,

CC i.e. proteins, polypeptides and peptides expressed in association with

CC the tumor and it encodes nucleic acids for said proteins, polypeptides and

SQ Sequence 390 BP; 101 A; 99 C; 87 G; 102 T; 0 U; 1 Other;

Query Match 19.2%; Score 176.6; DB 3; Length 390;
Best Local Similarity 93.0%; Pred. No. 2.1e-43;
Matches 185; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 328 ACCTCTGCTGTGGCCAATGCAGGAATGCTGGCCATCATTGCTTCTGCTGGGCGACTGAGA 387
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 264 ATCTCTGCTGTGGCCAATGCAGGAATGCTGGCCATCATTGCTTCTGCTGGGCGACTGAGA 205

Qy 388 AGCATCACCCACTTCCCCAGAACCTTTTTTACGTGGAGTGAAAACCTTTAAGGGGCTGTCC 447
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 204 AGCATCACCCACTTCCCCAGAACCTTTTTTACGTGGAGTGAAAACCTTTAAGGGGCTGTCC 145

Qy 448 AGCTAAACCTCCAACCTCCAGATCCCATGCCAATTTCTCTGCTTCTGCAAAGGACTTCA 507
 ||||||||||||||||||||| |||||||||||||||||||||||||||||
 Db 144 AGCTAAACCTCCAACCTCCAGATWCCATGCCAATTTCTCTGCTTCTGCAAAGGACTCAT 85

Qy 508 AGTGAAAGACATCTGCAGC 526
 | | | ||| ||||
 Db 84 GGGCAGCGTTATCCACAGC 66

ADY36463

ID ADY36463 standard; DNA; 561 BP.

AC ADY36463;

DT 05-MAY-2005 (first entry)

DE HIRA genomic fragment SEQ ID NO 108.

KW hybridization; DNA detection; neoplasm; genetic disorder; cytogenetics;
KW HIRA; ds.

OS Homo sapiens.

PN WO200188089-A2.

PD 22-NOV-2001.

XX

PF 15-MAY-2001; 2001WO-US015674.

XX

PR 16-MAY-2000; 2000US-00573080.

PR 14-MAY-2001; 2001US-00854867.

XX

PA (CHIL-) CHILDREN'S MERCY HOSPITAL.

XX

PI Knoll JHM, Rogan PK, Cazarro PM;

XX

DR WPI; 2002-062378/08.

XX

PT Single copy genomic hybridization probes for detecting specific nucleic
PT acid sequences in sample by in situ hybridization useful for detection of
PT acquired or inherited genetic diseases.

XX

PS Example 1; SEQ ID NO 108; 67pp; English.

XX

CC The invention describes a nucleic acid hybridization probe (I) comprising
CC a labeled, single copy nucleic acids of at least 50 nucleotides, which
CC will hybridize to a deduced single copy sequence interval in target
CC nucleic acid (TNA) of known sequence. (I) is useful in a hybridization
CC method which comprises preparing a reaction mixture comprising TNA and
CC (I) which hybridizes to TNA, and causing (I) to hybridize to TNA, where
CC the hybridization method is from in situ hybridization, Southern blot,
CC and other methods in which nucleic acid is immobilized, where the method
CC further comprises selecting a single copy nucleic acid which will
CC hybridize to a duplicon or triplicon sequence domain. (I) is useful for:
CC determining the existence of previously unknown repeat sequence families
CC in a genome; determining a chromosome breakpoint and in the fields of
CC cytogenetics and molecular genetics for determining the presence of
CC specific nucleic acid sequences in a sample of eukaryotic origin, e.g.
CC the probes may be used to analyze specific chromosomal locations by in
CC situ hybridization as a detection of acquired or inherited genetic
CC diseases especially for detection of genetic or neoplastic disorders.
CC Unlike prior art techniques, (I) permits more precise chromosomal
CC breakpoint determinations by in situ hybridization. Hybridization
CC techniques utilizing (I), have made it possible to obtain reliable,
CC easily detectable signals with relatively small probes. A readily
CC detectable signal was obtained with a probe on the order of 2 kb in
CC length, using fluorescent in situ hybridization (FISH) technology. This
CC sensitivity of (I) is improved compared to the prior art, because the
CC probes of (I) are homogeneous single copy sequences. However, smaller
CC amplified segments, each comprising non-repetitive sequences, may also be
CC used in combination as probes to achieve adequate signals for in situ
CC hybridization. Complex single copy probes that hybridize to duplicated or
CC triplicated targets can also increase hybridization signals. This
CC sequence represents a human HIRA genomic sequence that shows homology to
CC a known high-complexity repeat sequence family of the human genome and is

CC used in the creation of an HIRA gene probe.
XX
SQ Sequence 561 BP; 146 A; 146 C; 124 G; 141 T; 0 U; 4 Other;

Query Match 13.3%; Score 122.6; DB 1; Length 561;
Best Local Similarity 69.6%; Pred. No. 1.3e-26;
Matches 201; Conservative 0; Mismatches 74; Indels 14; Gaps 2;

Qy 2 CTGTAGAGGGGAATGGCTGCTGTGTCATGGGGGTGCATGAGCAGCCCAGTGGAGAGGTGC 61
 || | | || ||||| ||||| || | ||||| || ||||| |
Db 201 CTCTGGGGGAAGCCAGCTGCCATGTCATGAGGACACTCAAGCAGCCCTGTGGAGAGGCC 260

Qy 62 ACTTGGTGAGAAACCGATGCCT-CTGCCAACCACTGCACTAACCTGCTGGGTC----- 114
 | ||| || ||| || ||||| ||||| || || ||| | ||| | ||
Db 261 ATGTGGCAAGGAACTGAGGCCTCCTGCCAACAGCCAGCAAGGAACTGAGGCCTCCTGCCA 320

Qy 115 -----TGAGACTGAGCCACTTTGGAAGCTGATCTTGGAGCACCAGTCAAGCCCTTAGC 167
 || || ||||| ||||| ||||| | || ||||| ||||| | ||
Db 321 ACAGCCATGTGAGTGAGCCATCTTGGAAGCAGATCCTCCAGCCCCAGTCAAGCCTTCAGA 380

Qy 168 TGGCTGCAGCCACAGCCAACAACAAGACTGCAACCTCCTGGGGGATCCTGAGCCAGAATC 227
 || ||||| || ||| |||| | ||||| ||||| || | || ||||| ||||| |
Db 381 TGACTGCAGCCCCAGCTAACATCTTGACTGCAACCTCATGAGAGACCCTGAGCCAGAACC 440

Qy 228 CCCTGGCTAAATTGCTCCTTGATTCTTAACCCACAGAAATTGTGTAAGA 276
 || ||||| ||||| |||| | ||||| ||||| |||| |||
Db 441 ACCCAGCTAAGCTGCTCCTAAATTCCTGACCCACAGAACTGTGAGAGA 489

RESULT 6
ADS31075
ID ADS31075 standard; DNA; 561 BP.
XX
AC ADS31075;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human genome high complexity repeat found in the HIRA gene #108.
XX
KW Human; ds;
KW histone cell cycle regulation defective, S. cerevisiae homologue A; HIRA;
KW high complexity repeat; in situ hybridisation; Southern blot;
KW chromosome breakpoint; inherited genetic disease; neoplastic disorder;
KW chromosome 22; DiGeorge syndrome; Velo-Cardio-facial syndrome.
XX
OS Homo sapiens.
XX
PN US2003224356-A1.
XX

PD 04-DEC-2003.
XX
PF 14-MAY-2001; 2001US-00854867.
XX
PR 16-MAY-2000; 2000US-00573080.
XX
PA (KNOL/) KNOLL J H M.
PA (ROGA/) ROGAN P K.
XX
PI Knoll JHM, Rogan PK;
XX
DR WPI; 2002-062378/08.
XX
PT Single copy genomic hybridization probes for detecting specific nucleic
PT acid sequences in sample by in situ hybridization useful for detection of
PT acquired or inherited genetic diseases.
XX
PS Example 1; SEQ ID NO 108; 30pp; English.
XX
CC The invention relates to a nucleic acid hybridisation probe comprising a
CC labelled, single copy nucleic acids of at least 50 nucleotides, which
CC will hybridise to a deduced single copy sequence interval in target
CC nucleic acid (TNA) of known sequence. The single copy sequence is deduced
CC by comparing the target nucleic acid (e.g. a disease causing gene) with a
CC collection of high and low complexity repeat sequences as found in the
CC genome of the organism from containing the target nucleic acid. The probe
CC is generated by PCR on the target sequence. The probe is essentially free
CC of blocking nucleic acid sequences which will hybridise to repeat
CC sequences within the genome of which the TNA is a part, and is labelled
CC with a label selected from fluorochrome-responsive labels, fluorochromes,
CC calorimetric chemical, conjugated proteins, antibodies, antigens and
CC their mixtures. The probe is useful in a hybridisation method, where the
CC hybridisation method is from in situ hybridisation, Southern blot, and
CC other methods in which nucleic acid is immobilised, where the method
CC further comprises selecting a single copy nucleic acid which will
CC hybridise to a duplicon or triplicon sequence domain. The probe is useful
CC for determining the existence of previously unknown repeat sequence
CC families in a genome. The method comprises reacting a labelled probe with
CC the genome, causing the probe to hybridise and ascertaining if the probe
CC hybridises to the genome at more than three preferably ten different
CC locations as a determination of new repeat sequence family, where the
CC determining step comprises selecting the single copy sequence from a
CC duplicon or triplicon sequence domain. The probe is useful for
CC determining a chromosome breakpoint and is useful in the fields for
CC cytogenetics and molecular genetics for determining the presence of
CC specific nucleic acid sequences in a sample of eukaryotic origin, e.g.
CC the probes may be used to analyse specific chromosomal locations by in
CC situ hybridisation as a detection of acquired or inherited genetic
CC diseases especially for detection of genetic or neoplastic disorders.

CC Unlike prior art techniques, the probe permits more precise chromosomal
CC breakpoint determinations by in situ hybridisation. The genomic sequence
CC comprising the human HIRA gene (histone cell cycle regulation defective,
CC *S. cerevisiae*, homologue A) was analysed for single copy sequence
CC intervals for use as probes of the invention. HIRA is located on
CC chromosome 22 as a duplicate, deletions of 1 copy lead to DiGeorge and
CC Velo-Cardio-facial syndromes. The present sequence is a high complexity
CC repeat found within the human genome used to analyse the HIRA gene for
CC repeat regions. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030224356.
XX
SQ Sequence 561 BP; 146 A; 146 C; 124 G; 141 T; 0 U; 4 Other;

Query Match 13.3%; Score 122.6; DB 1; Length 561;
Best Local Similarity 69.6%; Pred. No. 1.3e-26;
Matches 201; Conservative 0; Mismatches 74; Indels 14; Gaps 2;

Qy 2 CTGTAGAGGGGAATGGCTGCTGTGTCATGGGGGTGCATGAGCAGCCCAGTGGAGAGGTGC 61
|| | | || |||| | |||| | | | |||| | |||| |
Db 201 CTCTGGGGGAAGCCAGCTGCCATGTCATGAGGACACTCAAGCAGCCCTGTGGAGAGGCC 260

Qy 62 ACTTGGTGAGAAACCGATGCCT-CTGCCAACCCACCTGCACTAACCTGCTGGGTC----- 114
| ||| || ||| || |||| | |||| | ||| | ||| |
Db 261 ATGTGGCAAGGAAGTGAAGCCTCCTGCCAACAGCCAGCAAGGAAGTGAAGCCTCCTGCCA 320

Qy 115 -----TGAGACTGAGCCACTTTGGAAGCTGATCTTGGAGCACCCAGTCAAGCCCTTAGC 167
|| || |||| | |||| | ||| | ||| |||| | ||
Db 321 ACAGCCATGTGAGTGAGCCATCTTGGAAGCAGATCCTCCAGCCCCAGTCAAGCCTTCAGA 380

Qy 168 TGGCTGCAGCCACAGCCAACAACAAGACTGCAACCTCCTGGGGGATCCTGAGCCAGAATC 227
|| |||| | ||| ||| | |||| | || | || |||| |
Db 381 TGACTGCAGCCCCAGCTAACATCTTGACTGCAACCTCATGAGAGACCCTGAGCCAGAACC 440

Qy 228 CCCTGGCTAAATTGCTCCTTGATTCTTAACCCACAGAAATTGTGTAAGA 276
|| |||| | |||| | ||| | |||| | ||| |||
Db 441 ACCCAGCTAAGCTGCTCCTAAATTCCTGACCCACAGAAACTGTGAGAGA 489

RESULT 7
ADY36462
ID ADY36462 standard; DNA; 541 BP.
XX
AC ADY36462;
XX
DT 05-MAY-2005 (first entry)
XX
DE HIRA genomic fragment SEQ ID NO 107.
XX

KW hybridization; DNA detection; neoplasm; genetic disorder; cytogenetics;
KW HIRA; ds.
XX
OS Homo sapiens.
XX
PN WO200188089-A2.
XX
PD 22-NOV-2001.
XX
PF 15-MAY-2001; 2001WO-US015674.
XX
PR 16-MAY-2000; 2000US-00573080.
PR 14-MAY-2001; 2001US-00854867.
XX
PA (CHIL-) CHILDREN'S MERCY HOSPITAL.
XX
PI Knoll JHM, Rogan PK, Cazarro PM;
XX
DR WPI; 2002-062378/08.
XX
PT Single copy genomic hybridization probes for detecting specific nucleic
PT acid sequences in sample by in situ hybridization useful for detection of
PT acquired or inherited genetic diseases.
XX
PS Example 1; SEQ ID NO 107; 67pp; English.
XX
CC The invention describes a nucleic acid hybridization probe (I) comprising
CC a labeled, single copy nucleic acids of at least 50 nucleotides, which
CC will hybridize to a deduced single copy sequence interval in target
CC nucleic acid (TNA) of known sequence. (I) is useful in a hybridization
CC method which comprises preparing a reaction mixture comprising TNA and
CC (I) which hybridizes to TNA, and causing (I) to hybridize to TNA, where
CC the hybridization method is from in situ hybridization, Southern blot,
CC and other methods in which nucleic acid is immobilized, where the method
CC further comprises selecting a single copy nucleic acid which will
CC hybridize to a duplicon or triplicon sequence domain. (I) is useful for:
CC determining the existence of previously unknown repeat sequence families
CC in a genome; determining a chromosome breakpoint and in the fields of
CC cytogenetics and molecular genetics for determining the presence of
CC specific nucleic acid sequences in a sample of eukaryotic origin, e.g.
CC the probes may be used to analyze specific chromosomal locations by in
CC situ hybridization as a detection of acquired or inherited genetic
CC diseases especially for detection of genetic or neoplastic disorders.
CC Unlike prior art techniques, (I) permits more precise chromosomal
CC breakpoint determinations by in situ hybridization. Hybridization
CC techniques utilizing (I), have made it possible to obtain reliable,
CC easily detectable signals with relatively small probes. A readily
CC detectable signal was obtained with a probe on the order of 2 kb in
CC length, using fluorescent in situ hybridization (FISH) technology. This

CC sensitivity of (I) is improved compared to the prior art, because the
CC probes of (I) are homogeneous single copy sequences. However, smaller
CC amplified segments, each comprising non-repetitive sequences, may also be
CC used in combination as probes to achieve adequate signals for in situ
CC hybridization. Complex single copy probes that hybridize to duplicated or
CC triplicated targets can also increase hybridization signals. This
CC sequence represents a human HIRA genomic sequence that shows homology to
CC a known high-complexity repeat sequence family of the human genome and is
CC used in the creation of an HIRA gene probe.

XX

SQ Sequence 541 BP; 135 A; 137 C; 123 G; 126 T; 0 U; 20 Other;

Query Match 13.2%; Score 121.2; DB 1; Length 541;
Best Local Similarity 68.8%; Pred. No. 3.5e-26;
Matches 190; Conservative 3; Mismatches 81; Indels 2; Gaps 2;

Qy 2 CTGTAGAGGGGAATGGCTGCTGTGTCATGGGGGTGCATGAGCAGCCCAGTGGAGAGGTGC 61
||| ||| ||||| || ||| | | ||||| | ||||| |||
Db 197 CTCTGGGGGAAGCCAGCTGCCATGCTATGAAGACACTCAAGCAGCCTA-TGGAGAAGTCC 255

Qy 62 ACTTGGTGAGAAACCGATGCCT-CTGCCAACCACCTGCACTAACCTGCTGGGTCTGAGAC 120
|| ||| || ||| || | || ||||| || || ||: ||| | || ||
Db 256 ACGTGGSAAGGAAGTCTCCTGCCAACAGCCAGCTTCGACYTGCCAGCCATGTGAG 315

Qy 121 TGAGCCACTTTGGAAGCTGATCTTGGAGCACCAAGTCAAGCCCTTAGCTGGCTGCAGCCAC 180
||||| ||||| |||| | ||| |||||: |||| | || || ||||| |
Db 316 TGAGCCATCTTGGAAGCGGATCCTCCAGCCCCAGTYAAGCCTTCAGATGACTGCAGCCCC 375

Qy 181 AGCCAACAACAAGACTGCAACCTCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATT 240
|| ||| | ||||| ||||| || | || ||||| ||||| || ||||| |
Db 376 GGCTGACATCTTGACTGCAACCTCATGAGAGACCCTGAGCCAGAACTACCCAGCTAAGCT 435

Qy 241 GCTCCTTGATTCTTAACCCACAGAAATTGTGTAAGA 276
||||| : |||| | ||||| |||| | || |
Db 436 GCTCCTARATTCCTGACCCACAGAACTGTGAGATA 471

RESULT 8
ADS31074
ID ADS31074 standard; DNA; 541 BP.
XX
AC ADS31074;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human genome high complexity repeat found in the HIRA gene #107.
XX
KW Human; ds;
KW histone cell cycle regulation defective, S. cerevisiae homologue A; HIRA;

KW high complexity repeat; in situ hybridisation; Southern blot;
 KW chromosome breakpoint; inherited genetic disease; neoplastic disorder;
 KW chromosome 22; DiGeorge syndrome; Velo-Cardio-facial syndrome.
 XX
 OS Homo sapiens.
 XX
 PN US2003224356-A1.
 XX
 PD 04-DEC-2003.
 XX
 PF 14-MAY-2001; 2001US-00854867.
 XX
 PR 16-MAY-2000; 2000US-00573080.
 XX
 PA (KNOL/) KNOLL J H M.
 PA (ROGA/) ROGAN P K.
 XX
 PI Knoll JHM, Rogan PK;
 XX
 DR WPI; 2002-062378/08.
 XX
 PT Single copy genomic hybridization probes for detecting specific nucleic
 PT acid sequences in sample by in situ hybridization useful for detection of
 PT acquired or inherited genetic diseases.
 XX
 PS Example 1; SEQ ID NO 107; 30pp; English.
 XX
 CC The invention relates to a nucleic acid hybridisation probe comprising a
 CC labelled, single copy nucleic acids of at least 50 nucleotides, which
 CC will hybridise to a deduced single copy sequence interval in target
 CC nucleic acid (TNA) of known sequence. The single copy sequence is deduced
 CC by comparing the target nucleic acid (e.g. a disease causing gene) with a
 CC collection of high and low complexity repeat sequences as found in the
 CC genome of the organism from containing the target nucleic acid. The probe
 CC is generated by PCR on the target sequence. The probe is essentially free
 CC of blocking nucleic acid sequences which will hybridise to repeat
 CC sequences within the genome of which the TNA is a part, and is labelled
 CC with a label selected from fluorochrome-responsive labels, fluorochromes,
 CC calorimetric chemical, conjugated proteins, antibodies, antigens and
 CC their mixtures. The probe is useful in a hybridisation method, where the
 CC hybridisation method is from in situ hybridisation, Southern blot, and
 CC other methods in which nucleic acid is immobilised, where the method
 CC further comprises selecting a single copy nucleic acid which will
 CC hybridise to a duplicon or triplicon sequence domain. The probe is useful
 CC for determining the existence of previously unknown repeat sequence
 CC families in a genome. The method comprises reacting a labelled probe with
 CC the genome, causing the probe to hybridise and ascertaining if the probe
 CC hybridises to the genome at more than three preferably ten different
 CC locations as a determination of new repeat sequence family, where the

Query Match 13.2%; Score 121.2; DB 1; Length 541;
Best Local Similarity 68.8%; Pred. No. 3.5e-26;
Matches 190; Conservative 3; Mismatches 81; Indels 2; Gaps 2;

Qy	2	CTGTAGAGGGGAATGGCTGCTGTGTTCATGGGGGTGCATGAGCAGCCCACTGGAGAGGTGC	61
Db	197	CTCTGGGGGAAGCCAGCTGCCATGCTATGAAGACACTCAAGCAGCCTA-TGGAGAAGTCC	255
Qy	62	ACTTGGTGAGAAACCGATGCCT-CTGCCAACCACTGCACTAACCTGCTGGGTCTGAGAC	120
Db	256	ACGTGGSAAAGGAAGTCTCCTGCCAACAGCCAGCTTCGACYTGCCAGCCATGTGAG	315
Qy	121	TGAGCCACTTTGGAAGCTGATCTTGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCAC	180
Db	316	TGAGCCATCTTGGAAGCGGATCCTCCAGCCCCAGTYAAGCCTTCAGATGACTGCAGCCCC	375
Qy	181	AGCCAACAACAAGACTGCAACCTCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATT	240
Db	376	GGCTGACATCTTGACTGCAACCTCATGAGAGACCCTGAGCCAGAACTACCCAGCTAAGCT	435
Qy	241	GCTCCTTGATTCTTAACCCACAGAAATTGTGTAAGA	276
Db	436	GCTCCTARATTCTTGACCCACAGAACTGTGAGATA	471

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ID ADC20771 standard; DNA; 737 BP.
 XX
 AC ADC20771;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human secreted protein-related DNA sequence #189.
 XX
 KW gene therapy; human; secreted protein; haemopoietic disorder;
 KW haematological disorder; anaemia; haemophilia; inflammatory disorder;
 KW inflammatory bowel disease; Crohn's disease; neoplastic disease; cancer;
 KW leukaemia; wound healing; epithelial cell proliferation disorder;
 KW immune disorder; autoimmune disorder; asthmatic disorder;
 KW cardiovascular disorder; atherosclerosis; myocarditis;
 KW infectious disease; HIV; AIDS; endocrine disorder; diabetes;
 KW gastrointestinal disorder; duodenal ulcer; gastroenteritis; gene; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200292787-A2.
 XX
 PD 21-NOV-2002.
 XX
 PF 26-MAR-2002; 2002WO-US009257.
 XX
 PR 27-MAR-2001; 2001US-0278650P.
 PR 12-SEP-2001; 2001US-00950082.
 PR 12-SEP-2001; 2001US-00950083.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Ruben SM;
 XX
 DR WPI; 2003-129287/12.
 XX
 PT New human secreted proteins and nucleic acid molecules, useful for
 PT preparing a diagnostic or pharmaceutical composition for diagnosing,
 PT preventing or treating hematopoietic or hematologic disorders, e.g.
 PT anemia or hemophilia.
 XX
 PS Disclosure; SEQ ID NO 725; 1512pp; English.
 XX
 CC The invention comprises the amino acid and coding sequences of human
 CC secreted proteins. The DNA and protein sequences of the invention are
 CC useful for detecting, preventing, diagnosing, prognosticating, treating
 CC or ameliorating: haematopoietic or haematological disorders (e.g. anaemia
 CC and haemophilia); inflammatory disorders (e.g. inflammatory bowel disease
 CC and Crohn's disease); neoplastic disease (e.g. cancer and leukaemia);
 CC wound healing and disorders of epithelial cell proliferation; immune

CC disorders (e.g. autoimmune disorders and asthmatic disorders);
CC cardiovascular disorders (e.g. atherosclerosis and myocarditis);
CC infectious disease (e.g. HIV/AIDS); endocrine disorders (e.g. diabetes);
CC and gastrointestinal disorders (e.g. duodenal ulcers and
CC gastroenteritis). The present DNA sequence was used in the
CC exemplification of the invention.
XX
SQ Sequence 737 BP; 198 A; 174 C; 148 G; 217 T; 0 U; 0 Other;

Query Match 11.4%; Score 104.8; DB 1; Length 737;
Best Local Similarity 68.5%; Pred. No. 4.9e-21;
Matches 174; Conservative 0; Mismatches 77; Indels 3; Gaps 2;

Qy 24 TGTCATGGGGGTGCATGAGCAGCCCAGTGGAGAGGTGCACTTGGTGAGAAACCGATGCCT 83
| ||||| || | | |||| || ||||| | || ||||| ||||| || |||||
Db 398 TTTCATGAGGATACTCAAGCATTCTATGGAGAGATCCACATGGTGAGAAACTGAAGCCT 457

Qy 84 -CTGCCAACCACCTGCACTAACCTGCTGGGTCTGAGACTGAGCCACTTTGGAAGCTGATC 142
|| |||| || |||| ||| ||| | | || ||||| || |||| | |
Db 458 CCTACCAAGAGCCAGCACCAACTTGCCAGCTATGTGAATGAGCCATCTTAGAAGTGGGTT 517

Qy 143 TTGGAGCACCAAGTCAAGCCCTTAGCTGGCTGCAGCCACAGCCAACAACAAGACTGCAACC 202
| ||| | |||| ||| | | || ||||| || | | |||| |||||
Db 518 CTCTAGCCCTAGTCAGGCCTTCATATGACTGCAGCCAGGGCTGATATTTTGACTACAACC 577

Qy 203 TCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATTGCTCCTTGATTCTTAACCCACA 262
|| || | || ||||| || || ||||| ||||| |||| ||| |||
Db 578 TCATGAGAGA--CTGAGCCACAACAACCTAGCTAAGAAGCTCCTGAATTCCTACCAACA 635

Qy 263 GAAATTGTGTAAGA 276
|||| | ||| |||
Db 636 GAAACTATGTGAGA 649

RESULT 10
ADA44374
ID ADA44374 standard; DNA; 737 BP.
XX
AC ADA44374;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human secreted protein DNA SEQ ID 567.
XX
KW Gene therapy; human; Antidiabetic; Anorectic; Ophthalmological;
KW Neuroprotective; Cerebroprotective; Antianemic; ds.
XX
OS Homo sapiens.
XX

PN WO2003000865-A2.
XX
PD 03-JAN-2003.
XX
PF 26-MAR-2002; 2002WO-US009105.
XX
PR 27-MAR-2001; 2001US-0278650P.
PR 12-SEP-2001; 2001US-00950082.
PR 12-SEP-2001; 2001US-00950083.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2003-184045/18.
XX
PT A human secreted protein and nucleic acids useful for preparing a
PT diagnostic or pharmaceutical composition for diagnosing or treating
PT diabetes or conditions related to diabetes, e.g. hyperglycemia, obesity,
PT retinopathy, neuropathy.
XX
PS Disclosure; SEQ ID NO 567; 701pp; English.
XX
CC The invention relates to novel genes and their fragments which are useful
CC for preventing, treating or ameliorating medical conditions e.g. by
CC protein or gene therapy. The genes are isolated from a range of human
CC tissues disclosed in the specification. The nucleic acids and proteins
CC are useful in the diagnosis, treatment and prevention of conditions
CC related to diabetes, e.g. hyperglycaemia, obesity, retinopathy,
CC polyneuropathy, atherosclerosis, anaemia, stroke, gangrene, impotence,
CC infection, cataract, renal disorders, or endocrine disorders. The present
CC sequence was used to illustrate the invention.
XX
SQ Sequence 737 BP; 198 A; 174 C; 148 G; 217 T; 0 U; 0 Other;

Query Match 11.4%; Score 104.8; DB 1; Length 737;
Best Local Similarity 68.5%; Pred. No. 4.9e-21;
Matches 174; Conservative 0; Mismatches 77; Indels 3; Gaps 2;

Qy 24 TGTCATGGGGGTGCATGAGCAGCCCAGTGGAGAGGTGCACTTGGTGAGAAACCGATGCCT 83
| ||||| || | | |||| || ||||| | ||| ||||| || ||||
Db 398 TTTCATGAGGATACTCAAGCATTCTATGGAGAGATCCACATGGTGAGAAACTGAAGCCT 457

Qy 84 -CTGCCAACCACCTGCACTAACCTGCTGGGTCTGAGACTGAGCCACTTTGGAAGCTGATC 142
|| |||| || |||| ||| ||| | | || ||||| || |||| | |
Db 458 CCTACCAAGAGCCAGCACCAACTTGCCAGCTATGTGAATGAGCCATCTTAGAAGTGGGTT 517

Qy 143 TTGGAGCACCAAGTCAAGCCCTTAGCTGGCTGCAGCCACAGCCAACAACAAGACTGCAACC 202
| ||| | |||| ||| | | || ||||| || | | |||| ||||

Db 518 CTCTAGCCCTAGTCAGGCCTTCATATGACTGCAGCCAGGGCTGATATTTTGACTACAACC 577

Qy 203 TCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATTGCTCCTTGATTCTTAACCCACA 262
|| || | || ||||| || || |||| ||||| ||| |||

Db 578 TCATGAGAGA--CTGAGCCACAACAACCTAGCTAAGAAGCTCCTGAATTCCTACCAACA 635

Qy 263 GAAATTGTGTAAGA 276
|||| | ||| |||

Db 636 GAAACTATGTGAGA 649

RESULT 11

ADF10918

ID ADF10918 standard; DNA; 737 BP.

XX

AC ADF10918;

XX

DT 12-FEB-2004 (first entry)

XX

DE Human secreted protein encoding sequence #240.

XX

KW H6EDM64; HBHAA05; HBJCR46; HBJKD16; HCMSX51; HCQBH72; HDPPQ30; HE2CM39;

KW HE9EA10; HGBHP91; HLDQU79; Cytostatic; Hepatotropic; Antidiabetic;

KW Antiinflammatory; neuroprotective; Anti-HIV; Vulnerary; Gynecological;

KW Antiinfertility; Gene therapy; gastrointestinal disorder; cancer;

KW Alzheimer's disease; chromosome identification; ds.

XX

OS Homo sapiens.

XX

PN WO200299085-A2.

XX

PD 12-DEC-2002.

XX

PF 26-MAR-2002; 2002WO-US009135.

XX

PR 27-MAR-2001; 2001US-0278650P.

PR 12-SEP-2001; 2001US-00950082.

PR 12-SEP-2001; 2001US-00950083.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Rosen CA, Ruben SM;

XX

DR WPI; 2003-221310/21.

XX

PT New human secreted polypeptides for diagnosing and treating neural,
PT immune system, muscular, reproductive, gastrointestinal, cardiovascular,
PT renal, and proliferative disorders and cancerous diseases.

XX

Qy 263 GAAATTGTGTAAGA 276
|||| | ||| |||
Db 636 GAAACTATGTGAGA 649

RESULT 12

ADA98650

ID ADA98650 standard; DNA; 737 BP.

XX

AC ADA98650;

XX

DT 20-NOV-2003 (first entry)

XX

DE Human secreted protein-related DNA sequence #243.

XX

KW human; secreted protein; cardiovascular disorder; arrhythmia;
KW atherosclerosis; stroke; endocarditis; congestive heart failure;
KW rheumatic heart disease; cardiomyopathy; hemorrhoids; varicose veins;
KW migraine; thrombosis; neural disorder; immune system disorder;
KW muscular disorder; reproductive disorder; gastrointestinal disorder;
KW pulmonary disorder; renal disorder; proliferative disorder; cancer; ds.

XX

OS Homo sapiens.

XX

PN WO2003004623-A2.

XX

PD 16-JAN-2003.

XX

PF 26-MAR-2002; 2002WO-US009922.

XX

PR 27-MAR-2001; 2001US-0278650P.

PR 12-SEP-2001; 2001US-00950082.

PR 12-SEP-2001; 2001US-00950083.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Rosen CA, Ruben SM;

XX

DR WPI; 2003-247946/24.

XX

PT New human secreted polypeptide and nucleic acid molecules, useful for
PT diagnosing, preventing, prognosticating or treating cardiovascular
PT disorders (e.g. arrhythmia, atherosclerosis, cardiomyopathy, or
PT thrombosis).

XX

PS Disclosure; SEQ ID NO 759; 1572pp; English.

XX

CC The invention comprises the amino acid and coding sequence of human
CC secreted proteins. The DNA and protein sequences of the invention are

CC useful in the treatment of cardiovascular disorders, such as: arrhythmia,
CC atherosclerosis, stroke, endocarditis, congestive heart failure,
CC rheumatic heart disease, cardiomyopathy, hemorrhoids, varicose veins,
CC migraine, or thrombosis. The DNA and protein sequences may also be used
CC for treating or preventing: neural disorders, immune system disorders,
CC muscular disorders, reproductive disorders, gastrointestinal disorders,
CC pulmonary disorders, renal disorders, proliferative disorders and/or
CC cancerous diseases. The present DNA sequence is used in the
CC exemplification of the invention. NOTE: The present sequence is shown on
CC the WIPO website.
XX
SQ Sequence 737 BP; 198 A; 174 C; 148 G; 217 T; 0 U; 0 Other;

Query Match 11.4%; Score 104.8; DB 1; Length 737;
Best Local Similarity 68.5%; Pred. No. 4.9e-21;
Matches 174; Conservative 0; Mismatches 77; Indels 3; Gaps 2;

Qy 24 TGTCATGGGGGTGCATGAGCAGCCCAGTGGAGAGGTGCACTTGGTGAGAAACCGATGCCT 83
| ||||| || | | |||| || ||||| | ||| ||||| || ||||
Db 398 TTTCATGAGGATACTCAAGCATTCTATGGAGAGATCCACATGGTGAGAAACTGAAGCCT 457

Qy 84 -CTGCCAACCACCTGCACTAACCTGCTGGGTCTGAGACTGAGCCACTTTGGAAGCTGATC 142
|| |||| || |||| ||| ||| | | || ||||| || |||| | |
Db 458 CCTACCAAGAGCCAGCACCAACTTGCCAGCTATGTGAATGAGCCATCTTAGAAGTGGGTT 517

Qy 143 TTGGAGCACCAAGTCAAGCCCTTAGCTGGCTGCAGCCACAGCCAACAACAAGACTGCAACC 202
| ||| | |||| ||| | | || ||||| || | | |||| ||||
Db 518 CTCTAGCCCTAGTCAGGCCTTCATATGACTGCAGCCAGGGCTGATATTTTGACTACAACC 577

Qy 203 TCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATTGCTCCTTGATTCTTAACCCACA 262
|| || | || ||||| || || ||| |||| ||||| |||| ||| |||
Db 578 TCATGAGAGA--CTGAGCCACAACAACCTAGCTAAGAAGCTCCTGAATTCCTACCAACA 635

Qy 263 GAAATTGTGTAAGA 276
|||| | ||| |||
Db 636 GAAACTATGTGAGA 649

RESULT 13
AOD72587
ID AOD72587 standard; cDNA; 737 BP.
XX
AC AOD72587;
XX
DT 01-MAY-2008 (first entry)
XX
DE Human secreted protein cDNA sequence, SEQ ID 6677.
XX
KW therapy; cancer; cytostatic; immune disorder; immunomodulator;

KW hematological disease; antianemic; reproduction disorder;
KW musculoskeletal disease; muscular-gen.; osteopathic;
KW genitourinary disease; uropathic; neurological disease; neuroprotective;
KW respiratory disease; respiratory-gen.; endocrine disease; endocrine-gen.;
KW gastrointestinal disease; gastrointestinal-gen.; gene; ss.
XX
OS Homo sapiens.
XX
PN US2007032413-A1.
XX
PD 08-FEB-2007.
XX
PF 26-MAR-2002; 2002US-00105299.
XX
PR 26-MAR-2002; 2002US-00105299.
XX
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2007-341847/32.
XX
PT New isolated human secreted proteins, useful for detecting, preventing,
PT diagnosing, prognosticating, treating, or ameliorating diseases and
PT disorders related to the proteins, e.g. cancers, reproductive, or
PT cardiovascular diseases.
XX
PS Example 1; SEQ ID NO 6677; 339pp; English.
XX
CC The present invention relates to human secreted polypeptides and their
CC coding sequences. Also claimed are: a composition comprising the
CC polypeptide and a carrier; and an isolated protein produced by (a)
CC expressing the polypeptide by a cell; and (b) recovering the protein.
CC Also disclosed as new are: antibodies that bind these polypeptides;
CC vectors; host cells; recombinant and synthetic methods for producing the
CC polynucleotides, polypeptides, and/or antibodies; screening methods for
CC identifying agonists and antagonists of polynucleotides and polypeptides;
CC and methods and compositions for inhibiting or enhancing the production
CC and function of the polypeptides. The polypeptides are useful for
CC detecting, preventing, diagnosing, prognosticating, treating, and/or
CC ameliorating diseases and disorders related to the proteins or
CC polypeptides. Diseases and disorders include cancers;
CC immune/hematopoietic disorders (e.g. anemia, pancytopenia, leukopenia,
CC thrombocytopenia, or plasmacytomas); reproductive disorders (e.g.
CC cryptorchism, prostatitis, inguinal hernia, varicocele, or leydig cell
CC tumors); musculoskeletal disorders (e.g. osteochondromas, benign
CC chondromas, Paget's disease, or rheumatoid arthritis); cardiovascular
CC diseases (e.g. heart failure, congestive heart disease, arrhythmia,

Query Match 11.4%; Score 104.8; DB 3; Length 737;
Best Local Similarity 68.5%; Pred. No. 4.9e-21;
Matches 174; Conservative 0; Mismatches 77; Indels 3; Gaps 2;

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RESULT 14
AAC79717
ID      AAC79717 standard; cDNA; 797 BP.
XX
AC      AAC79717;
XX
DT      12-FEB-2001   (first entry)
```

XX
DE Human secreted protein gene 37 SEQ ID NO:47.
XX
KW Human; secreted protein; diagnosis; cytostatic; immunosuppressive;
KW nootropic; neuroprotective; antiviral; antiallergic; hepatotropic;
KW antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant;
KW antibacterial; antifungal; antiparasitic; cardiant; gene therapy;
KW food additive; preservative; chromosome identification; cancer;
KW immune disorder; cardiovascular disorder; neurological disease;
KW wound healing; infectious disease; ss.
XX
OS Homo sapiens.
XX
PN WO200058339-A2.
XX
PD 05-OCT-2000.
XX
PF 22-MAR-2000; 2000WO-US007440.
XX
PR 26-MAR-1999; 99US-0126503P.
PR 17-DEC-1999; 99US-0172409P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM, Komatsoulis G;
XX
DR WPI; 2000-594637/56.
DR P-PSDB; AAB44632.
XX
PT Fifty nucleic acid molecules encoding human secreted proteins, useful in
PT the prevention, treatment and diagnosis of cancer, immune disorders,
PT cardiovascular disorders and neurological diseases.
XX
PS Claim 1; Page 357-358; 410pp; English.
XX
CC The polynucleotide sequences given in AAC79681 to AAC79730 encode the
CC human secreted proteins given in AAB44596 to AAB44645. AAB44646 to
CC AAB44693 represent human secreted polypeptide sequences and proteins
CC homologous to them, which are given in the exemplification of the present
CC invention. Human secreted proteins have activities based on the tissues
CC and cells the genes are expressed in. Examples of activities include:
CC cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
CC antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
CC vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; and
CC cardiant. The polynucleotides and polypeptides are useful for preventing,
CC treating or ameliorating a medical condition in e.g. humans, mice,
CC rabbits, goats, horses, cats, dogs, chickens or sheep. The polypeptides
CC can also be used as a food additive or preservative to increase or
CC decrease storage capabilities. The polynucleotides are useful for

Query Match 11.4%; Score 104.8; DB 1; Length 797;
Best Local Similarity 68.5%; Pred. No. 5e-21;
Matches 174; Conservative 0; Mismatches 77; Indels 3; Gaps 2;

Qy	24	TGTCATGGGGGTGCATGAGCAGCCAGTGGAGAGGTGCACTTGGTGAGAAACCGATGCCT	83
Db	383	TTTCATGAGGATACTCAAGCATTCTATGGAGAGATCCACATGGTGAGAAACTGAAGCCT	442
Qy	84	-CTGCCAACCACCTGCACTAACCTGCTGGGTCTGAGACTGAGCCACTTTGGAAGCTGATC	142
Db	443	CCTACCAAGAGCCAGCACCAACTTGCCAGCTATGTGAATGAGCCATCTTAGAAGTGGGT	502
Qy	143	TTGGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCACAGCCAACAACAAGACTGCAACC	202
Db	503	CTCTAGCCCTAGTCAGGCCTTCATATGACTGCAGCCAGGGCTGATATTTTGACTACAACC	562
Qy	203	TCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATTGCTCCTTGATTCTTAACCCACA	262
Db	563	TCATGAGAGA--CTGAGCCACAACAACCTAGCTAAGAAGCTCCTGAATTCCCTACCAACA	620
Qy	263	GAAATTGTGTAAGA	276
Db	621	GAAACTATGTGAGA	634

ADC20168

XX

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XX

XX

KW haematological disorder; anaemia; haemophilia; inflammatory disorder;

KW inflammatory bowel disease; Crohn's disease; neoplastic disease; cancer;
 KW leukaemia; wound healing; epithelial cell proliferation disorder;
 KW immune disorder; autoimmune disorder; asthmatic disorder;
 KW cardiovascular disorder; atherosclerosis; myocarditis;
 KW infectious disease; HIV; AIDS; endocrine disorder; diabetes;
 KW gastrointestinal disorder; duodenal ulcer; gastroenteritis; gene; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200292787-A2.
 XX
 PD 21-NOV-2002.
 XX
 PF 26-MAR-2002; 2002WO-US009257.
 XX
 PR 27-MAR-2001; 2001US-0278650P.
 PR 12-SEP-2001; 2001US-00950082.
 PR 12-SEP-2001; 2001US-00950083.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Ruben SM;
 XX
 DR WPI; 2003-129287/12.
 XX
 PT New human secreted proteins and nucleic acid molecules, useful for
 PT preparing a diagnostic or pharmaceutical composition for diagnosing,
 PT preventing or treating hematopoietic or hematologic disorders, e.g.
 PT anemia or hemophilia.
 XX
 PS Claim 1; SEQ ID NO 117; 1512pp; English.
 XX
 CC The invention comprises the amino acid and coding sequences of human
 CC secreted proteins. The DNA and protein sequences of the invention are
 CC useful for detecting, preventing, diagnosing, prognosticating, treating
 CC or ameliorating: haematopoietic or haematological disorders (e.g. anaemia
 CC and haemophilia); inflammatory disorders (e.g. inflammatory bowel disease
 CC and Crohn's disease); neoplastic disease (e.g. cancer and leukaemia);
 CC wound healing and disorders of epithelial cell proliferation; immune
 CC disorders (e.g. autoimmune disorders and asthmatic disorders);
 CC cardiovascular disorders (e.g. atherosclerosis and myocarditis);
 CC infectious disease (e.g. HIV/AIDS); endocrine disorders (e.g. diabetes);
 CC and gastrointestinal disorders (e.g. duodenal ulcers and
 CC gastroenteritis). The present DNA sequence encodes a human secreted
 CC protein of the invention.
 XX
 SQ Sequence 797 BP; 269 A; 173 C; 149 G; 206 T; 0 U; 0 Other;

Query Match 11.4%; Score 104.8; DB 1; Length 797;

